

(SEQ ID NO.: 15 shown in 5' to 3' direction and SEQ ID NO.: 1 shown in the 3' to 5' direction).

Figure 2 shows the amino acid sequence of three fingers used for phage display selection in the determination of recognition code, in which F1 is set forth SEQ ID NO.: 16, F2 randomization at position 6 is set forth in SEQ ID NO.: 17 and F3 randomizations at residue positions -1 and 2 are set forth in SEQ ID No.: 18 and randomizations at residue positions -1 to 3 are set forth in SEQ ID No.: 19.

Figure 3 lists the sequence-specific zinc finger clones obtained from phage selections, and their binding site signatures, corresponding to SEQ IS NOs.: 20-114.

*Figures 4a and 4b*  
~~Figure 4~~ shows the nitrogenous base/amino acid correlation of the clones isolated from phage selections. Recognition patterns are highlighted.

*Sub D1*  
Figure 5 illustrates the sequence-specific interactions selected at position 2 of the  $\alpha$ -helix, binding to position 1 of the quadruplet, for which sequence identifiers are shown.

Figure 6 is a schematic diagram of the construction of a library according to the invention, in which SEQ ID NO.: 14 is set forth in the 3' to 5' direction.

**IN THE FIGURES:**

*(12)*  
Kindly replace the originally filed Figure 3 with the attached informally revised Figure 3 for examination purposes. Revisions to the Figure are set forth in red.

**IN THE SEQUENCE LISTING:**

*Sub C2*  
Please enter the attached substitute Sequence Listing in lieu of the Sequence Listing submitted on March 7, 2001.